INSTITUTE FOR BRAIN AND NEURAL SYSTEMS

June 30, 1993

Dr. Joel L. Davis, Program Manager
Office of Naval Research
Code 1142 BI
800 N. Quincy Street
Arlington, Virginia 22217-5000

Re: Progress Report N00014-91-J-1316

Dear Dr. Davis:

This is written to provide a semi-annual progress report for the contract N00014-91-J-1316 entitled "Theoretical and Experimental Research into Biological Mechanisms Underlying Learning and Memory." The major goal of our research is to elucidate the biological mechanisms that underlie learning and memory: to find principles of organization that can account both for experimental data on the cellular level and, when applied to large numbers of neurons that receive sensory and/or interneuronal information, for various higher level system properties.

Among our detailed objectives are the following: to clarify the dependence of learning on synaptic modification, to elucidate the principles that govern synapse formation or modification, to use principles of organization that can account for observations on a cellular level to construct neural-like systems that can learn, associate and reproduce such higher level cognitive acts as abstraction and computation.

The approaches employed to achieve these objectives include both theory and experiment. Theoretical and experimental consequences of the hypothesis that synapse modification is dependent on local information (in visual cortex, dominated by the inputs from the eyes with specific visual information) in accordance with theoretical ideas we have developed, as well as by global instructions affecting large numbers of synapses and coming perhaps from modulatory transmitters such as norepinephrine, have been tested. In addition, various principles that appear to be operating on the cellular level have been used to construct models of higher level functions.

One of our key objectives is to produce real interaction between theory and experiment. The means for achieving this has been a continuing dialogue between experimentalists and theoreticians that has produced a genuine collegial relationship in which experts in very different disciplines can understand each other's language.

1 Simulations using natural inputs

A key simplification used up to now in simulations and analysis of the evolution of BCM neurons has been the visual environment. In the past contract period we have begun and investigation of the validity of this rearing environment model used in the CBC simulations of visual deprivation experiments was tested by using a more realistic model of visual experience. Natural images preprocessed by a retinal filter were used to generate input to a single cell model of synaptic plasticity in visual cortex. The simulations of normal rearing, monocular deprivation and reverse suture using these realistic inputs produced similar results as the CBC simulations which used abstract one dimensional inputs.

These simulations used a model of the kitten visual system from the retina to primary visual cortex. A single neuron represented the cortex, and the BCM theory was used to model its synaptic plasticity. Circular regions from the left and the right retinas covering the same visual space, were used to generate input to the single BCM neuron. The lateral geniculate nucleus (LGN) was assumed to simply relay the signal generated by the retina to the visual cortex.

Each retina included an array of ganglion cells spaced one unit apart, and an array of receptors which were also spaced one unit apart. Only ganglion cells, whose receptive-field midpoints fell within a circular visual area with a radius of five units were included in the model. Each ganglion cell had an antagonistic center-surround receptive field which approximated a difference of two Gaussians. The standard deviation of the center Gaussian was 1 unit, and the standard deviation of the surround Gaussian was 3 units. This created a receptive field center with a radius of 2.22 units. The receptive field of each ganglion cell was balanced so that uniform illumination of any intensity resulted in spontaneous activity.

The visual environment of the model consisted of eight gray scale images with dimensions 150X150 pixels. For each cycle of the simulation, the activity of the receptors in the retina was determined by randomly picking one of the eight images, and randomly shifting the image on the models retina. The shift was restricted so that none of the ganglion cell receptive field centers fell within five units of the image border. The activity of each receptor in the model was determined by the intensity of a pixel in the image. This method generated a very large training set because of the many unique shifts which were possible. The maximum ganglion cell activity generated by the patterned input was 1.57, and the ganglion cell activity generated by a sutured eye was simply noise uniformly distributed in the interval $[0.0, 0.8)$.

A selected times during the simulations, spots of light were used to characterize the receptive field of the BCM neuron through the left and right eyes. Two dimensional maps of the

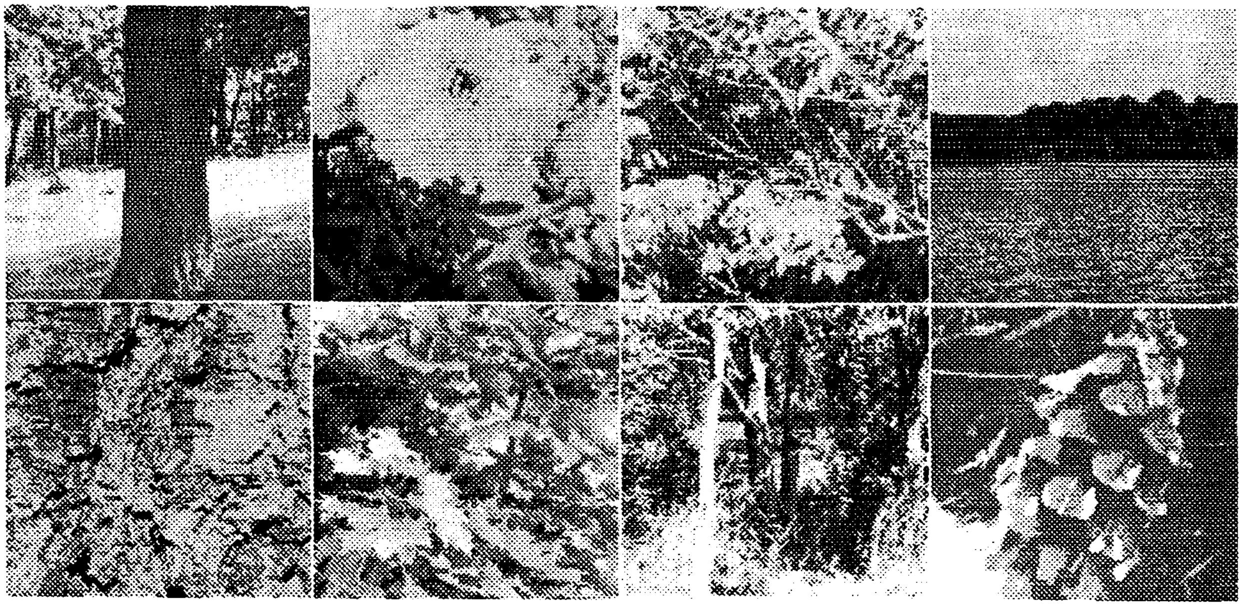

Figure 1: Natural images used for training the model.

receptive field were generated by "shining" small spots of light at many location on a retina and recording the BCM activity generated for each spot. This is similar to the process used by Palmer and Jones to generate two-dimensional receptive field profiles of simple cells in cat striate cortex (Jones and Palmer, 1987). The maximums of the left eye map and the right eye map were used to determine the binocularity of the BCM neuron.

Figures 3, 5 and 7 show the results from simulations of normal rearing, monocular deprivation and reverse suture. They can be compared to the results of the CBC simulations shown in figures 2, 4 and 6. The scale of the horizontal axis in these two sets of figures is different because the simulations using the natural input required many more training iterations for the BCM neuron to become selective. This can be accounted for by the additional complexity introduced by the realistic input. As in the CBC simulations, normal rearing produced a binocular neuron which was equally driven through the left and the right eyes. The two-dimensional maps of the BCM neurons receptive field show how it also develops selectivity to the orientation of a stimulus.

In both simulations of monocular deprivation, the sutured eye disconnects from the BCM neuron, and in both simulations of reverse suture the newly closed eye disconnects from the BCM neuron before the newly open eye reconnects. These results suggest that the original abstract patterns distorted by noise were an adequate model of visual experience for the simulations of these visual deprivation experiments.

2 Localized Principal Components of Natural Images - an Analytic Solution

It has been proven that a neuron with Hebbian learning rule plus a proper decay term can perform a principal component extraction. Furthermore, a neural network with proper lateral inhibition can perform the extraction of several principal components simultaneously. The computational importance of principal components is that they are the optimal linear projections for minimizing the mean squared reconstruction error.

Since the principal components of a set of inputs depend only on their covariance matrix, it is reasonable that given this matrix, they can be calculated analytically.

We believe that it is reasonable to model postnatel development with an environment composed of natural scenes. The nature of the covariance matrix of natural images was investigated by Field, who found that the spectrum of covariance matrix is proportional to the inverse of the square of the frequency.

We assume a circular hard boundary to the receptive fields, with a radius equal to the zero crossing of the correlation function.

We find that the solutions are the Fourier-Bessel functions. We will show in section 3, that under the assumption that the covariance matrix spectrum has a small non-rotationally symmetric correction, the solutions have a definite phase.

2.1 The Rotationally Symmetric Solution

The principal components are the eigen-functions of the covariance matrix. Therefore the equation we try to solve is the eigenvalue problem, i.e., the eigen-equation, which has the form

$$\sum_j C_{ij} W_j = \lambda W_i \tag{1}$$

where W_i are eigen-vectors, λ is the eigenvalue, and C_{ij} is the covariance matrix which is defined as $C_{ij} = E[(I_i - E[I_i])(I_j - E[I_j])]$ for input pattern $\{I_i\}$. Since we are dealing with two dimensional space, the index i really denotes a point in the two dimensional space, so it is more convenient to rewrite the covariance matrix in the form $C(\mathbf{r}_i, \mathbf{r}'_j)$. Due to translational invariance, $C(\mathbf{r}_i, \mathbf{r}'_j) = C(\mathbf{r}_i - \mathbf{r}'_j)$. In the continuous limit, the summation will become an integral over $\mathbf{r}'$, thus the eigen-equation becomes

$$\int C(\mathbf{r} - \mathbf{r}')\psi(\mathbf{r}')d^2\mathbf{r}' = \lambda\psi(\mathbf{r}). \tag{2}$$

in which $w(\mathbf{r})$ is the continuous limit of the eigen-vectors W_i.

The Fourier transform (spectrum) of the covariance matrix has the form, $C(\mathbf{k}) = c/\mathbf{k}^2$ where c is a constant. Hereafter we will set $c = 1$ for convenience. Thus $C(\mathbf{r})$ satisfies

$$\nabla^2 C(\mathbf{r} - \mathbf{r}') = -\delta(\mathbf{r} - \mathbf{r}'). \tag{3}$$

which can be readily proven by taking Fourier transformation on both side of this equation. Since the correlation function is zero on some boundery assumed to be a circuler boundery of radius a, then within this boundery it can be represented as a sum of a complete set of functions with the same boundery condition. We will choose the Bessel Fourier set W_{mi} which is zero on the boundery, which take the form

$$W_{mi}(\mathbf{r}) = \begin{cases} J_m(\frac{r}{\sqrt{\lambda_{mi}}}) \begin{cases} cos(m\theta) \\ sin(m\theta) \end{cases} & \text{for } r \leq a \\ 0 & \text{for } r > a \end{cases} \tag{4}$$

in which $m = 0, 1, 2, \ldots$, $J_m(x)$ is the standard Bessel functions, λ_{mi} is the ith root of equation $J_m(a/\sqrt{\lambda}) = 0$, r and θ are the polar coordinates of $\mathbf{r}$. These functions solve the differential equation,

$$\nabla^2 W_{im} = -(1/\lambda_{mi}) W_{im}. \tag{5}$$

In this representation the correlation function must take the form

$$C(\mathbf{r} - \mathbf{r}') = \sum_{im} \lambda_{im} W^*_{im}(\mathbf{r}) W_{im}(\mathbf{r}') \tag{6}$$

Since, remembering that $\delta(\mathbf{r} - \mathbf{r}') = \sum_{kl} W^*_{kl}(\mathbf{r}) W_{kl}(\mathbf{r}')$, it is easy to see that $C(\mathbf{r} - \mathbf{r}')$ is a solution of eq:3. It is important to notice that this solution to $C(\mathbf{r} - \mathbf{r}')$ is not unique, since we can add a constant to this and still retain a radially symmetric equation. This is avoided by choosing the boundery a such that this constant is 0, which implies that the hard wired connections between retina and neurons must have a spatial extent which is equal to the zero crossing of the correlation function.

Thus plugging the correlation function of eq:6 into the eigen equation, representing the eigenfunctions as well as sums of this complete set, $\psi(\mathbf{r}) = \sum_{jn} B_{jn} W_{jn}(\mathbf{r})$, and using the orthogonality of these functions over the interval, we obtain that

$$\sum_{kl} \lambda_{kl} B_{kl} W_{kl}(\mathbf{r}) = \lambda \sum_{kl} B_{kl} W_{kl}(\mathbf{r}).$$

For which the solution, is that only one of the coefficients $B_{ij} = 1$ and the rest are zero. The corresponding eigenvalue is $\lambda = \lambda_{ij}$. Thus the solutions are the Bessel Fourier functions.

$$\begin{aligned} w^1_{mi}(\mathbf{r}) &= \begin{cases} J_m(\frac{r}{\sqrt{\lambda_{mi}}}) cos(m\theta + \phi_{mi}) & \text{for } r \leq a \\ 0 & \text{for } r > a \end{cases} \\ w^2_{mi}(\mathbf{r}) &= \begin{cases} J_m(\frac{r}{\sqrt{\lambda_{mi}}}) sin(m\theta + \phi_{mi}) & \text{for } r \leq a \\ 0 & \text{for } r > a \end{cases} \end{aligned} \tag{7}$$

where ϕ_{mi} is a set of undetermined phases. These two eigen-functions have the same eigenvalue λ_{mi}, i.e., they are degenerate.

If we order the solutions by the magnitudes of the correspondent eigenvalues λ_{mi}, the first ten solutions, $w^1_{mi}(\mathbf{r})$ with $\phi_{mi} = 0$ and $a = 1$, are drawn in figure 8.

2.2 Retrieving the Phase

The solutions above $w^1_{mi}(\mathbf{r})$ and $w^2_{mi}(\mathbf{r})$ not only have undetermined phases, but also are degenerate. This contradicts the results of the simulationspreformed by Hancock in which the phases seem to always take the value zero, and the W^1_{mi} solution has a different eigenvalue from the W^2_{mi} solution. These results can be retrieved if we assume that the covariance matrix has a non-rotationally symmetric perturbation term. This assumption is not arbitrary since an inspection of Fields results reveals that this is indeed the case. Hereafter we assume this perturbation term has, in $\mathbf{k}$ space, the form

$$C'(\mathbf{k}) = U(k)T(\theta_{\mathbf{k}}). \tag{8}$$

In order to calculate this perturbation, the representation of this perturbation in the two degenerate eigen-functions $W^1_{mi}(\mathbf{r})$ and $W^2_{mi}(\mathbf{r})$ has to be calculated. It is easier to perform this in $\mathbf{k}$ space in which the eigen-functions $W^1_{mi}(\mathbf{r})$ and $W^2_{mi}(\mathbf{r})$ are replaced by their Fourier transforms,

$$\begin{aligned} W^1_{mi}(\mathbf{k}) &= f_{mi}(k)cos(m\theta_{\mathbf{k}} + \phi_{mi}) \\ W^2_{mi}(\mathbf{k}) &= f_{mi}(k)sin(m\theta_{\mathbf{k}} + \phi_{mi}) \end{aligned} \tag{9}$$

in which

$$f_{mi}(k) = \pi j^m \int_0^a J_m(\frac{r}{\sqrt{\lambda_{mi}}})J_m(kr)rdr \tag{10}$$

where $j^2 = -1$. If we denote

$$T(\theta_{\mathbf{k}}) = \sum_l t_l cos(l(\theta_{\mathbf{k}} - \alpha_l)) \tag{11}$$

which is the Fourier expansion of $T(\theta_{\mathbf{k}})$. The representation of the perturbation matrix with respect to the two degenerate eigen-functions has the form

$$\begin{aligned} (C'_{(\mu,m,i|\gamma,m,i)})_{(\mu=1,2|\gamma=1,2)} &= (\int W^{\mu}_{mi}(\mathbf{k})^* C'(\mathbf{k}) W^{\gamma}_{mi}(\mathbf{k}) d^2\mathbf{k})_{(\mu=1,2|\gamma=1,2)} \\ &= g_{mi} \begin{pmatrix} cos(\delta) & sin(\delta) \\ sin(\delta) & -cos(\delta) \end{pmatrix} \end{aligned} \tag{12}$$

in which $\delta = 2\phi_{mi} + 2m\alpha_{2m}$ and $g_{mi} = \frac{\pi}{2} t_{2m} \int U(k)|f_{mi}(k)|^2 kdk$. Since the two eigen-functions are degenerate, any linear combination of these two eigen-functions is an eigen-function of C. Therefore, all we have to do is to find a linear combination of them which diagonalizes the perturbation matrix, i.e., to find the eigenvalues and eigen-vectors of the matrix in equation 12, which are

$$\begin{gathered} \begin{pmatrix} cos(\delta/2) \\ sin(\delta/2) \end{pmatrix} \\ \\ \begin{pmatrix} -sin(\delta/2) \\ cos(\delta/2) \end{pmatrix} \end{gathered} \tag{13}$$

with eigenvalues g_{mi} and $-g_{mi}$ respectively. Furthermore, if $U(k) = \epsilon/k^2$ then the complete expression for the correction to the eigenvalue takes the form $g_{mi} = \epsilon\lambda_{mi}t_{2m}/2$.

Thus the eigen-functions and eigenvalues after the perturbation can be readily written out as

$$W^{+}_{mi}(\mathbf{k}) = J_m(\frac{r}{\sqrt{\lambda_{mi}}})cos(m(\theta - \alpha_{2m}))$$
$$W^{-}_{mi}(\mathbf{k}) = J_m(\frac{r}{\sqrt{\lambda_{mi}}})sin(m(\theta - \alpha_{2m})) \tag{14}$$

with eigenvalues $\lambda^{+}_{mi} = \lambda_{mi} + g_{mi}$, and $\lambda^{-}_{mi} = \lambda_{mi} - g_{mi}$, respectively. So the degeneracy is broken. This is in agreement with Hancock's simulations. These solutions have an important feature, i.e., their phases are determined by the properties of the real world covariance matrix. If the covariance matrix has a definite symmetry with an inclination angle α, then the solutions would also have the same symmetry angle. Because in this case $\alpha_{2m} = \alpha$ for all m. The spectrums of the covariance matrix, shown in figure 7 of Field's paper, indeed indicates a symmetry axis along $\alpha = 0$. Thus equation 14 predicts the zero phase result found in Hancock's simulation. When Hancock used images which were tilted by 45 degrees before being scanned, the preferred axis of the receptive fields was found to be 45 degrees. Again this is predicted by equation 14, because the symmetry axis of the covariance matrix spectrum also gets rotated by 45 degrees due to the rotated images, i.e., $\alpha = 45°$, and thus the solutions also get rotated by 45 degrees.

2.3 Discussion

We have calculated the forms of the principal components of natural images based on the result about the covariance matrix, and have shown that a non-rotationally symmetric perturbation can break the degeneracy and give a definite phase which only depends on the properties of the real world covariance matrix. These results for a large part agree with the numerical simulation.

The neurobiological relevance of the type of technique used in this paper is that we can deduce for different learning rules what kinds of receptive fields they should produce. Given these receptive fields, we can compare them to the real biological receptive fields. This comparison can be used to assess whether the biological hardware really implements or approximates a theoretically proposed learning rule.

The most obvious conclusion which stands out when we observe the results in figure 8, is that these receptive fields have little resemblance to receptive fields reported in the biological literature. Does this imply that biological neurons are not principal component analizers? When addressing this question we have to keep in mind that the natural images projected on the retina, undergo preprocessing in the retina and LGN, before they reach the visual cortex. Similar preprocessing should therefore be applied to natural images in simulations and analytic studies, before a sensible answer can be given.

3 Hybrid Network Techniques

We have previously shown that hybrid network techniques can significantly improve network performance on difficult real-world problems. Below, we develop a firm mathematical framework for the observed network performance improvement.

3.1 Basic Ensemble Method

Consider the following regression problem

$$y = f(x) + n$$

where y is a random variable with mean $f(x) = E[y|x]$ and n is independent zero-mean noise.[1] We present the Basic Ensemble Method (BEM) which combines a population of regression estimates, $\hat{f}_i(x)$, to estimate a function $f(x)$.

Suppose that we have two finite data sets whose elements are all independent and identically distributed random variables: a training data set $\mathcal{A} = \{(x_m, y_m)\}$ and a cross-validatory data set $\mathcal{CV} = \{(x_l, y_l)\}$. Further suppose that we have used $\mathcal{A}$ to generate a set of functions, $\mathcal{F} = f_i(x)$, each element of which approximates $f(x)$.[2] We would like to find the best approximation to $f(x)$ using $\mathcal{F}$.

One common choice is to use the *naive estimator*, $f_{\text{Naive}}(x)$, which minimizes the empirical mean square error relative to $f(x)$,[3]

$$\text{MSE}[f_i] = E_{\mathcal{CV}}[(y_l - f_i(x_l))^2],$$

thus

$$f_{\text{Naive}}(x) = \arg\min_i\{\text{MSE}[f_i]\}.$$

This choice is unsatisfactory for two reasons: First, in selecting only one regression estimate from the population of regression estimates represented by $\mathcal{F}$, we are discarding potentially useful information that is stored in the discarded regression estimates; second, since the $\mathcal{CV}$ data set is random, there is a certain probability that some other network from the population will perform better than the naive estimate on some other previously unseen data set sampled from the same distribution. A more reliable estimate of the performance on previously unseen data is the average of the performances over the population $\mathcal{F}$. Below, we will see how we can avoid both of these problems by using the BEM estimator, $f_{\text{BEM}}(x)$, and thereby generate an improved regression estimate.

[1] The noise for minimizing the MSE is assumed to be Gaussian; but this assumption is not necessary for what follows.

[2] For our purposes, it does not matter how $\mathcal{F}$ was generated, unlike Monte Carlo. In practice we will use a set of backpropagation networks trained on the $\mathcal{A}$ data set but started with different random weight configurations. This replication procedure is standard practice when trying to optimize neural networks.

[3] Here, and in all of that follows, the expected value is taken over the cross-validatory set $\mathcal{CV}$.

Define the *misfit* of function $f_i(x)$, the deviation from the true solution, as $m_i(x) \equiv f(x) - f_i(x)$. The empirical mean square error can now be written in terms of $m_i(x)$ as

$$\mathrm{MSE}[f_i] = E[m_i^2].$$

The average mean square error is therefore

$$\overline{\mathrm{MSE}} = \frac{1}{N}\sum_{i=1}^{N} E[m_i^2].$$

Define the BEM regression function, $f_{\mathrm{BEM}}(x)$, as

$$f_{\mathrm{BEM}}(x) \equiv \frac{1}{N}\sum_{i=1}^{N} f_i(x) = f(x) - \frac{1}{N}\sum_{i=1}^{N} m_i(x)$$

If we now assume that the $m_i(x)$ are mutually independent with zero mean, we can calculate the mean square error of $f_{\mathrm{BEM}}(x)$ as

$$\begin{aligned}
\mathrm{MSE}[f_{\mathrm{BEM}}] &= E\Big[\big(\frac{1}{N}\sum_{i=1}^{N} m_i\big)^2\Big] \\
&= \frac{1}{N^2}E\Big[\sum_{i=1}^{N} m_i^2\Big] + \frac{1}{N^2}E\Big[\sum_{i\neq j} m_i m_j\Big] \\
&= \frac{1}{N^2}E\Big[\sum_{i=1}^{N} m_i^2\Big] + \frac{1}{N^2}\sum_{i\neq j} E[m_i]E[m_j] \\
&= \frac{1}{N^2}E\Big[\sum_{i=1}^{N} m_i^2\Big],
\end{aligned} \tag{15}$$

which implies that

$$\mathrm{MSE}[f_{\mathrm{BEM}}] = \frac{1}{N}\overline{\mathrm{MSE}}. \tag{16}$$

This is a powerful result because it tells us that by averaging regression estimates, we can reduce our mean square error by a factor of N when compared to the population performance: By increasing the population size, we can in principle make the estimation error arbitrarily small! In practice however, as N gets large our assumptions on the misfits, $m_i(x)$, eventually breakdown. In particular, the assumption that $E[m_i m_j] = E[m_i]E[m_j]$ is no longer valid.

Consider the individual elements of the population $\mathcal{F}$. These estimators will more or less follow thc true regression function. If we think of the misfits functions as random noise functions added to the true regression function and these noise functions are uncorrelated with zero mean, then the averaging of the individual estimates is like averaging over the noise. In this sense, the ensemble method is smoothing in functional space and can be thought of as a regularizer with a smoothness assumption on the true regression function.

An additional benefit of the ensemble method's ability to combine multiple regression estimates is that the regression estimates can come from many different sources. This fact allows for flexibility in the application of the ensemble method. For example, the regression estimates can have different functional forms; or can be selected using different optimization (i.e. "training") algorithms; or can be selected by optimizing over different data sets. This last option - optimizing on different data sets - has important ramifications. One standard method for avoiding over-fitting during training is to use a cross-validatory hold-out set. The cross-validatory hold-out set is a subset of the total data available to us and is used to determine when to stop training. The hold-out data is not used to train. The problem is that since we use cross-validation to avoid over-fitting, each regression estimate is never trained on the hold-out data (i.e. the cross-validatory data set) and therefore, each regression estimate "sees" only part of the data and may be missing valuable information about the distribution of the data particularly if the total data set is small. This will always be the case for a single regression estimate using a cross-validatory stopping rule. However, this is not a problem for the ensemble estimator. When constructing our population, $\mathcal{F}$, we can train each regression estimate on the entire training set and let the smoothing property of the ensemble process remove any over-fitting or we can train each regression estimate in the population with a different split of training and hold-out data. In this way, the population as a whole will have seen the entire data set while each regression estimate has avoided over-fitting by using a cross-validatory stopping rule. Thus the ensemble estimator will see the entire data set while the naive estimator will not. In general, with this framework we can now easily extend the statistical jackknife, bootstrap and cross-validation techniques (Efron, 1982; Miller, 1974; Stone, 1974) to find better regression functions.

I would be happy to answer any questions you might have concerning this report.

Sincerely,

Leon N Cooper
Thomas J. Watson, Sr.
Professor of Science
Director, Institute for Brain and Neural Science

Enclosure: Publication List

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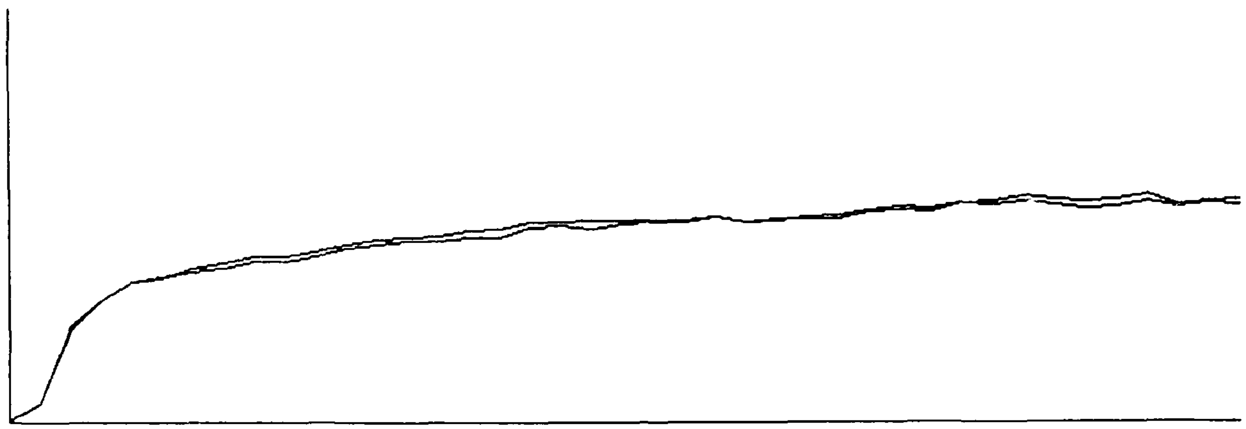

Figure 2: CBC simulation of normal rearing. The graph displays the maximum response to the training data for the left and right eyes.

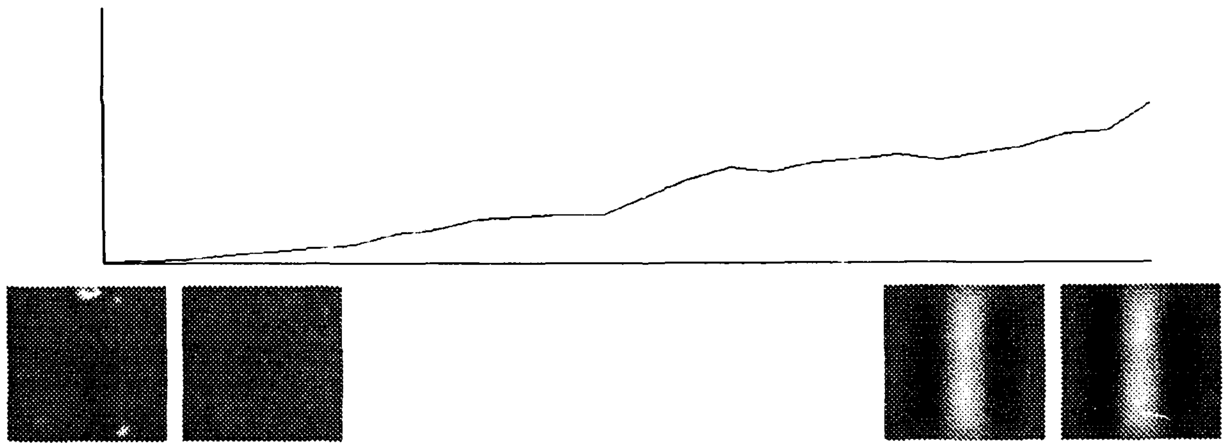

Figure 3: Simulation of normal rearing with realistic input. The 2d maps are the receptive fields for the left and right eyes at the beginning and end of the simulation. The upper graph shows the maximum of the left and right eye maps thoughout the simulation.

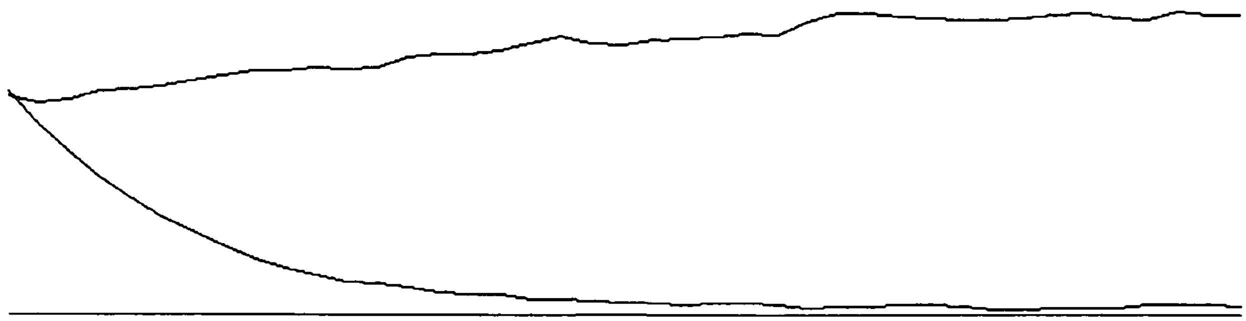

Figure 4: CBC simulation of monocular deprivation. The graph displays the maximum response to the training data for the left and right eyes.

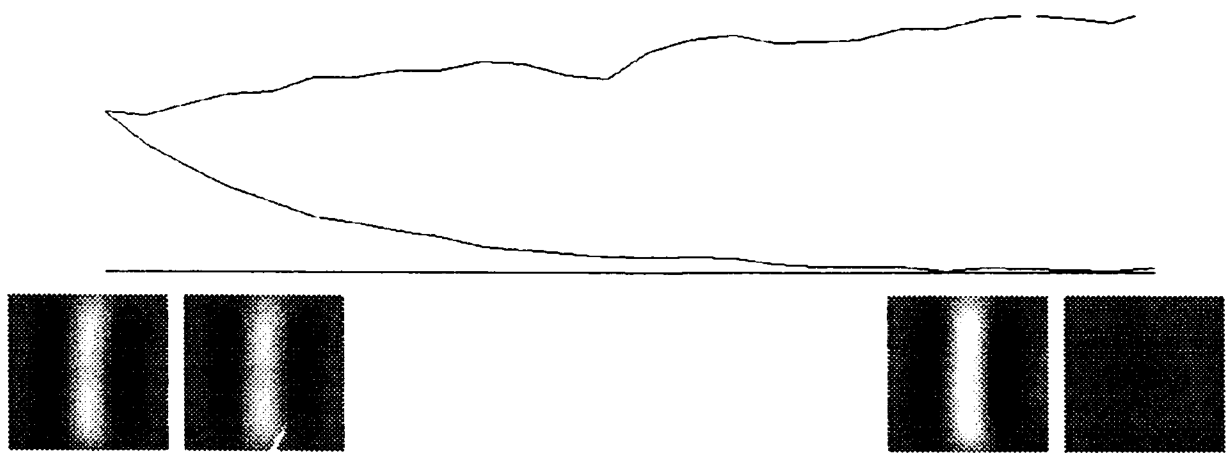

Figure 5: Simulation of monocular deprivation with realistic input. The 2d maps are the receptive fields for the left and right eyes at the beginning and end of the simulation. The upper graph shows the maximum of the left and right eye maps thoughout the simulation.

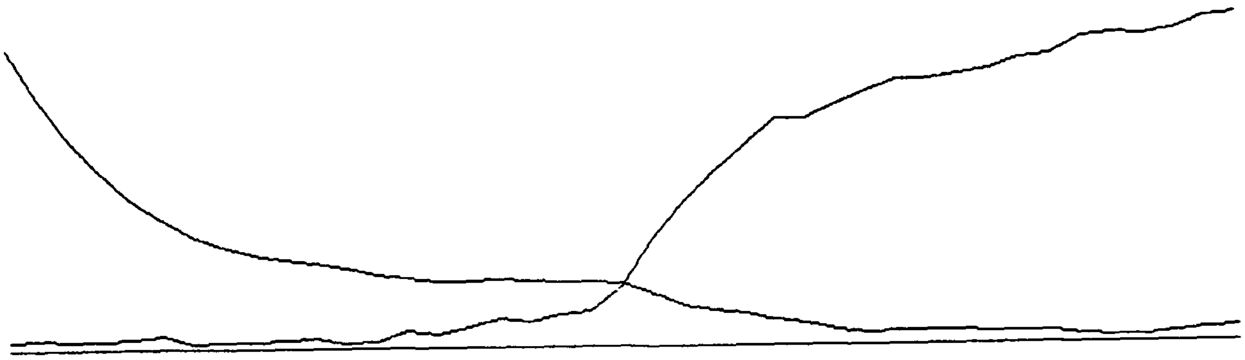

Figure 6: CBC simulation of reverse suture. The graph displays the maximum response to the training data for the left and right eyes.

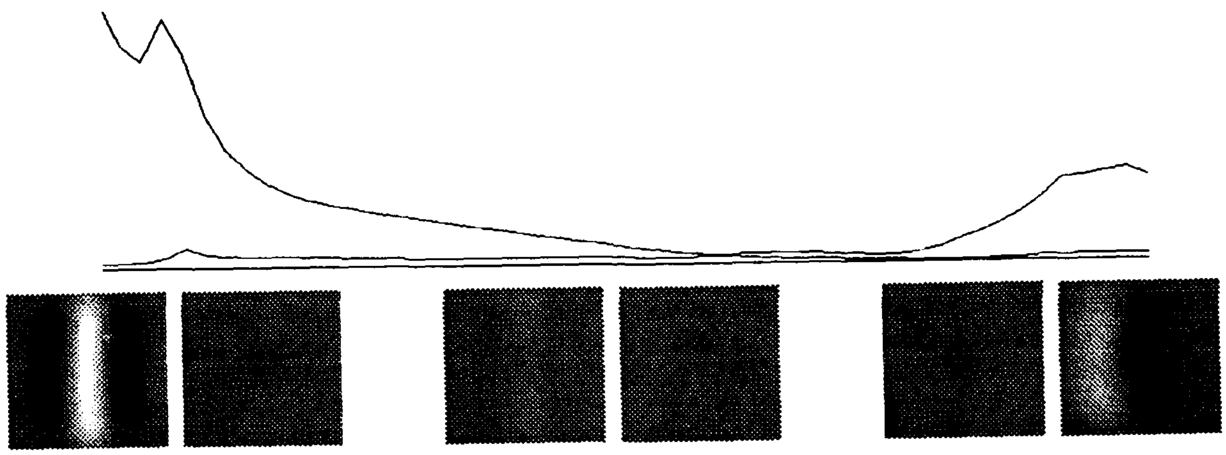

Figure 7: Simulation of reverse suture with realistic input. The 2d maps are the receptive fields for the left and right eyes at the beginning, middle and end of the simulation. The upper graph shows the maximum of the left and right eye maps thoughout the simulation.

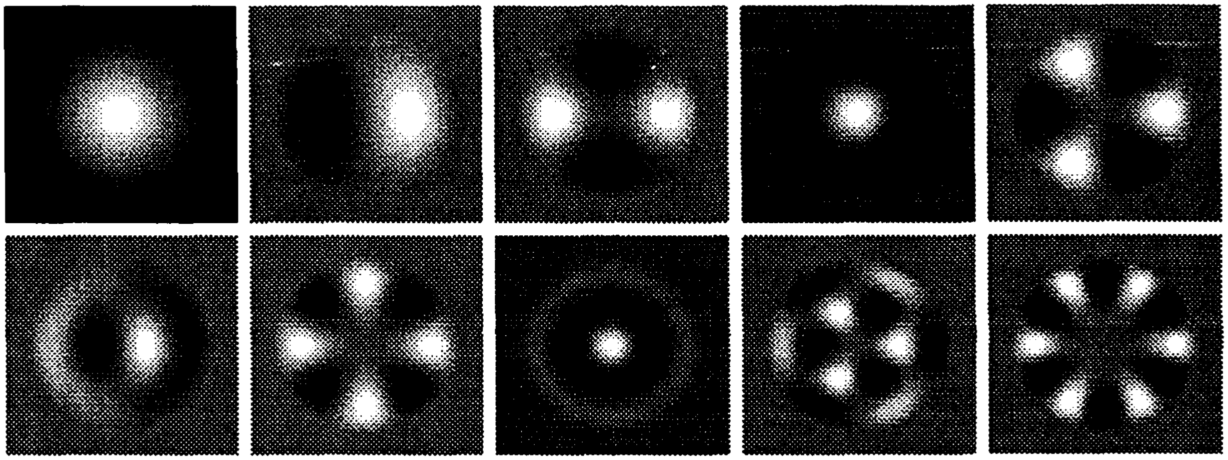

Figure 8: The shapes of the first ten principal components. ($W^1_{mi}(\mathbf{r})$ with $a = 1$ and $\phi_{mi} = 0$)

SOME ONR SUPPORTED PUBLICATIONS

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[2] J. A. Anderson. Cognitive and psychological computation with neural models. *IEEE Transactions on Systems, Man, and Cybernetics*, 13(5):799–815, 1983.

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